

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:17:40 ; Search time 71.77 Seconds
(without alignments)
27.514 Million cell updates/sec

Title: US-09-052-089a-5
Perfect score: 286
Sequence: 1 RALCTICSDPFDHSDVAA.....IOSFETAPSRICPCQRIQVG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	93	32.5	190	1 RNF4_HUMAN	P78317 homo sapien
2	93	32.5	194	1 RNF4_MOUSE	Q9QZS2 mus musculu
3	93	32.5	194	1 RNF4_RAT	O88846 rattus norv
4	92.5	32.3	624	1 A33_PLEVA	O02084 pleurodeles
5	88.5	30.9	411	1 RAPS_TORCA	P09108 torpedo cal
6	86	30.1	474	1 CBIC_HUMAN	O9ulv8 homo sapien
7	86	30.1	1238	1 YQO9_CAEEL	O09288 caenorhabdi
8	85.5	29.9	411	1 RAPS_CHICK	O42393 gallus gall
9	85.5	29.9	544	1 MKR3_MOUSE	O60764 mus musculu
10	84.5	29.5	411	1 RAPS_HUMAN	Q13702 homo sapien
11	84	29.4	513	1 REP_HUMAN	P14373 homo sapien
12	83.5	29.2	411	1 RAPS_MOUSE	P12672 mus musculu
13	83	29.0	235	1 YQ57_CAEEL	O09463 caenorhabdi
14	82	28.7	284	1 GOL1_DROME	O06003 drosophila
15	82	28.7	324	1 BM11_MOUSE	P25916 mus musculu
16	82	28.7	326	1 BM11_HUMAN	P35226 homo sapien
17	82	28.7	342	1 ME18_MOUSE	P33798 mus musculu
18	82	28.7	344	1 ME18_HUMAN	P35227 homo sapien
19	81.5	28.5	485	1 MKR4_HUMAN	Q13434 homo sapien
20	81	28.3	202	1 YP99_CAEEL	O09477 caenorhabdi
21	81	28.3	539	1 Z173_HUMAN	Q12899 homo sapien
22	81	28.3	634	1 Z147_MOUSE	O61510 mus musculu
23	80	28.0	906	1 CBL_HUMAN	P32681 homo sapien
24	79.5	27.8	161	1 YQUD_CAEEL	P30631 caenorhabdi
25	79	27.6	632	1 Z179_HUMAN	Q9ulv5 homo sapien
26	78	27.3	1281	1 YLB5_CAEEL	P46580 caenorhabdi
27	77	26.9	522	1 REP_MOUSE	O62118 mus musculu
28	77	26.9	917	1 STE5_YEAST	P32917 saccharomyc
29	77	26.9	982	1 CBLB_HUMAN	Q13191 homo sapien
30	76.5	26.7	416	1 MKR2_HUMAN	O9h000 homo sapien
31	76.5	26.7	416	1 MKR2_MOUSE	O9evr1 mus musculu
32	75.5	26.4	2025	1 TTC3_HUMAN	P33804 homo sapien
33	75	26.2	470	1 R052_MOUSE	O62191 mus musculu

34	75	26.2	631	1 Z179_RAT	O70418 rattus norv
35	73.5	25.7	409	1 YQ55_CAEEL	O09251 caenorhabdi
36	73.5	25.7	478	1 MKR1_MACEL	O9lt91 macropus eu
37	73.5	25.7	481	1 MKR1_MOUSE	O9qxp6 mus musculu
38	73.5	25.7	482	1 MKR1_HUMAN	O9unc7 homo sapien
39	73.5	25.7	585	1 YHBO_YEAST	P38748 saccharomyc
40	73	25.5	600	1 RNF1_MOUSE	O9wtv7 mus musculu
41	73	25.5	1562	1 YM81_YEAST	O04781 saccharomyc
42	72	25.2	482	1 RNF9_HUMAN	O9udv6 homo sapien
43	72	25.2	489	1 RNF9_MOUSE	O9wuh5 mus musculu
44	72	25.2	624	1 RNF2_HUMAN	O9nwv2 homo sapien
45	72	25.2	1169	1 RAD5_YEAST	P32849 saccharomyc

ALIGNMENTS

RESULT 1
ID RNF4_HUMAN STANDARD; PRT; 190 AA.
AC P78317;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RING finger protein 4.
GN RNF4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403881; PubMed=9734812;
RA Hadano S., Ishida Y., Ikeda J.E.;
RT "The primary structure and genomic organization of five novel transcripts located close to the Huntington's disease gene on human chromosome 4p16.3";
RT DNA Res. 5:177-186(1998).
RL [2]
RN SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
RP TISSUE=Brain;
RX MEDLINE=9810125; PubMed=9479498;
RA Chiarloti L., Benvenuto G., Fedele M., Santoro M., Simeone A., Fusco A., Bruni C.B.;
RT "Identification and characterization of a novel RING-finger gene (RNF4) mapping at 4p16.3";
RT Genomics 47:258-265(1998).
RL -1- FUNCTION: ENHANCES STEROID RECEPTOR-MEDIATED TRANSCRIPTIONAL ACTIVATION AS WELL AS ACTIVATING BASAL TRANSCRIPTION (BY SIMILARITY).
CC -1- SUBUNIT: INTERACTS WITH GSKL, ANDROGEN RECEPTOR AND TBP (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED AT LOW LEVELS IN MANY TISSUES; HIGHLY EXPRESSED IN TESTIS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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CC
CC EMBL; AB000468; BAA19122.1; -
CC EMBL; U95140; AAC52022.1; -
CC MIM: 602850; -
CC InterPro: IPR001841; Znf_Ring.
CC Pfam: PF00097; ZF-C3HC4; 1.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS00518; ZF_RING_1; 1.

DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Transcription regulation; Activator; Zinc-finger; Nuclear protein.
 FT ZN-FING 132 177 RING-TYPE.
 SO SEQUENCE 190 AA; 21319 MW; E5E3AE4A9B28CF9D CRC64.

Query Match 32.5%; Score 93; DB 1; Length 190;
 Best Local Similarity 37.3%; Pred. No. 7.4e-05;
 Matches 19; Conservative 8; Mismatches 18; Indels 6; Gaps 2;

OY 4 CTCI-----SDFPDHSRDVAAMDCGTHFLQCLIOSEFAPSPCTCCRIQV 50
 DB 132 CPICMDGYSEIVQNGRLIVSTECGHVFCSCQLRSLKNA--NTCPTCRKKI 180

RESULT 2
 RNF4_MOUSE STANDARD; PRT; 194 AA.
 AC Q9QZS2; Q35941;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RING finger protein 4.
 GN RNF4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Embryo;
 RX MEDLINE=20284895; PubMed=10822263;
 RA Gaili N., Nayak S., Epstein J.A., Buck C.A.;
 RT "Rnf4, a RING protein expressed in the developing nervous and
 reproductive systems, interacts with Gsc1, a gene within the DGeorge
 critical region.";
 RT Dev. Dyn. 218:102-111(2000).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CS7BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
 RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE OF 16-178 FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=98140125; PubMed=9479498;
 RA Chiarotti L., Benvenuto G., Fedele M., Santoro M., Simeone A.,
 RA Fusco A., Bruni C.B.;
 RT "Identification and characterization of a novel RING-finger gene
 (RNF4) mapping at 4p16.3.";

RL Genomics 47:258-265(1998).
 CC -1- ACTIVATION: ENHANCES STEROID RECEPTOR-MEDIATED TRANSCRIPTIONAL
 CC ACTIVATION AS WELL AS ACTIVATING BASAL TRANSCRIPTION (BY
 CC SIMILARITY)
 CC -1- SUBUNIT: INTERACTS WITH GSC1, ANDROGEN RECEPTOR AND TBP.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED PRIMARILY IN THE
 CC DEVELOPING NERVOUS SYSTEM WITH STRONG EXPRESSION IN THE DORSAL
 CC ROOT GANGLIA AND GONADS. UNBOUTHOUSLY EXPRESSED IN THE ADULT.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION IS DETECTED FROM EMBRYONIC DAY 7
 CC AND CONTINUES THROUGHOUT DEVELOPMENT AND INTO ADULTHOOD.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC -----
 DR EMBL; AF169300; AAR00620.1; -;
 DR EMBL; AK019171; BAB31585.1; -;
 DR EMBL; BC003282; AAH03282.1; -;
 DR EMBL; U95141; AAC53539.1; -;
 DR MGD; MGI:1201691; Rnf4.
 DR InterPro: IPR001841; Znf_Ring.
 DR Pfam; PF00097; ZF-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR SMART; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Transcription regulation; Activator; Zinc-finger; Nuclear protein.
 FT ZN-FING 136 181 RING-TYPE.
 SO SEQUENCE 194 AA; 21910 MW; 9A0A4277725C62E5 CRC64;

Query Match 32.5%; Score 93; DB 1; Length 194;
 Best Local Similarity 37.3%; Pred. No. 7.6e-05;
 Matches 19; Conservative 8; Mismatches 18; Indels 6; Gaps 2;

OY 4 CTCI-----SDFPDHSRDVAAMDCGTHFLQCLIOSEFAPSPCTCCRIQV 50
 DB 136 CPICMDGYSEIVQNGRLIVSTECGHVFCSCQLRSLKNA--NTCPTCRKKI 184

RESULT 3
 RNF4_RAT STANDARD; PRT; 194 AA.
 AC O68846;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RING finger protein 4 (SNURF).
 GN RNF4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98378525; PubMed=9710597;
 RA Mollanen A.-M., Poukka H., Karvonen U., Hakli M., Janne O.A.,
 RA Palvimäki J.U.;
 RT "Identification of a novel RING finger protein as a coregulator in
 RT steroid receptor-mediated gene transcription.";
 RT Mol. Cell. Biol. 18:5128-5139(1998).
 CC -1- FUNCTION: ENHANCES STEROID RECEPTOR-MEDIATED TRANSCRIPTIONAL
 CC ACTIVATION AS WELL AS ACTIVATING BASAL TRANSCRIPTION.
 CC -1- SUBUNIT: INTERACTS WITH GSC1, ANDROGEN RECEPTOR AND TBP.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN
 CC TESTIS.

RL J. Cell Biol. 107:1113-1121(1998).
 CC - FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
 CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
 CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON,
 CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
 CC - SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
 CC MEMBRANES.
 CC - ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO DISTINCT PROTEINS
 CC EXPRESSED, WHICH DIFFER IN THEIR C-TERMINUS.
 CC - DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
 CC REGULATOR DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
 CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
 CC - SIMILARITY: BELONGS TO THE RASVSN FAMILY.
 CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC -----
 DR EMBL: J02952; AAA49282.1; -;
 DR EMBL: J02953; AAA49283.1; -;
 DR PIR: A28009; A28009.
 DR InterPro: IPR001237; Postsynaptic.
 DR InterPro: IPR001440; TPR.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00515; TPR; 5.
 DR Pfam: PF00097; zf-G3HC4; 1.
 DR PRINTS: PR00217; POSTSYNAPTIC.
 DR PRODOM: PD012428; Postsynaptic; 1.
 DR SMART: SM00184; RING; 1.
 DR SMART: SM00028; TPR; 4.
 DR PROSITE: PS00405; 43_KD_POSTSYNAPTIC; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
 KW Myristate; Zinc-finger; Alternative splicing.
 FT INIT_MET 0
 FT ZN_FING 0
 FT LIPID 362 402 RING-TYPE.
 FT MOD_RES 1 1 MYRISTATE.
 FT MOD_RES 195 195 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 404 404 PHOSPHORYLATION (POTENTIAL).
 FT VARSPIC 389 411 MISSING (IN SHORT ISOFORM).
 FT CONFLICT 361 361 Y -> T (IN REF. 2).
 FT CONFLICT 393 393 N -> D (IN REF. 2).
 FT CONFLICT 410 410 Y -> T (IN REF. 2).
 SO SEQUENCE 411 AA; 46321 MW; 4D26262679FC9BAD CRC64;

 Query Match 30.9%; Score 88.5; DB 1; Length 411;
 Best Local Similarity 35.6%; Pred. No. 0.00058;
 Matches 16; Conservative 9; Mismatches 15; Indels 5; Gaps 2;

 Oy 4 CTTCSDFF-DHSRDVAAADCGHFLQCLISFETAPSRTCPCR 47
 | : : | : : | : | | | | | : | : | | : |
 Db 362 GGLGCESTIGDONSQDLALPCSHLFLKCLV---QTNGNRGCPNCK 402

 RESULT 6
 ID CBLC_HUMAN STANDARD; PRT; 474 AA.
 AC Q90LV8; Q9Y523; Q9Y522;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Signal transduction protein CBL-C (SH3-binding protein CBL-C) (CBL-3).
 GN CBLC OR CBL3.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A. (LONG FORM).
RX MEDLINE=20035821; PubMed=10571044;
RA Kim M., Tezuka T., Suzuki Y., Sugano S., Hirai M., Yamamoto T.;
RT "Molecular cloning and characterization of a novel cbl-family gene,
RL cbl-C."
RN Gene 239:145-154(1999).
RN [2]
RN SEQUENCE FROM N.A. (LONG AND SHORT FORMS).
RP TISSUE=Pancreatic adenocarcinoma;
RC MEDLINE=99289203; PubMed=10362357;
RA Keane M.M., Ettenberg S.A., Nau M.M., Banerjee P., Cuello M.,
RT Penninger J., Lipkowitz S.;
RL "cbl-3: a new mammalian cbl family protein."
CC Oncogene 18:3365-3375(1999).
CC -1- FUNCTION: REGULATOR OF EGFR MEDIATED SIGNAL TRANSDUCTION.
CC -1- SUBUNIT: INTERACTS WITH A RESTRICTED RANGE OF SH3 DOMAIN PROTEINS.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: UBIOUITOUS.
CC -1- PTM: PHOSPHORYLATED ON TYROSINES BY EGFR.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
CC CC
CC EMBL: AB028645; BAAB6298.1; -
CC DR EMBL: AF117646; AAD34341.1; -
CC DR EMBL: AF117647; AAD34342.1; -
CC DR HSSP: P22681; 1B47.
CC DR InterPro: IPR003153; Cbl_N.
CC DR InterPro: IPR000980; SH2.
CC DR InterPro: IPR001841; znf_fing.
CC DR Pfam: PF02262; Cbl_N; 1.
CC DR Pfam: PF02761; Cbl_N2; 1.
CC DR Pfam: PF02762; Cbl_N3; 1.
CC DR Pfam: PF00097; zf-C3HC4; 1.
CC DR Pfam: SM00184; RING; 1.
CC DR SMART: SM00252; SH2; 1.
CC DR PROSITE: PS00518; zf_RING_1; 1.
CC DR PROSITE: PS00889; zf_RING_2; 1.
CC KM Nuclear protein; zinc-finger; phosphorylation; alternative splicing.
CC FT DOMAIN 89 92
CC FT ZN_FING 351 390
CC FT VARSPLIT 261 306
CC FT CONFLICT 234 234
CC FT T -> N (IN REF. 2).
CC SEQUENCE 474 AA; 52468 MW; 91013BDF12828242 CRC64;

Query Match 30.1%; Score 86; DB 1; Length 474;
Best Local Similarity 33.3%; Pred. No. 0.0014;
Matches 16; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

OY 3 LCTTCSDFDHSRDVYAMDCGHTTHLQCLIOSFEFAPSRHTCPQCRIOY 50
Db 350 LCKICA--ESNKDVKIEPCGHLL-CSCCLAAMQHSDSQTCFPCRCFI 393

RESULT 7
ID Y009_CAEEL STANDARD; PRT; 1238 AA.
AC 009298;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical I41.2 kDa protein EEBED8.9 in chromosome II.

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DR EMBL: J03407; AAA36564.1; -
 DR PIR: A28101; TVHURF.
 DR MIM: 602165; -
 DR InterPro: IPR001870; Gamma_carboxylase.
 DR InterPro: IPR003877; SPRY.
 DR InterPro: IPR003878; SPRY_domain.
 DR InterPro: IPR00315; Znf_box.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00622; SPRY.1.
 DR Pfam: PF00643; Zf-B_box.1.
 DR Pfam: PF00097; Zf-C3HC4.1.
 DR PRINTS: PR01406; BBOX2NFINGER.
 DR SMART: SM00336; BBOX.1.
 DR SMART: SM00184; RING.1.
 DR SMART: SM00449; SPRY.1.
 DR PROSITE: PS50119; ZF_BOX.1.
 DR PROSITE: PS00518; ZF_RING.1.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR PROTO-ONCOGENE: Zinc-finger; Metal-binding; Chromosomal translocation;
 KM Nuclear protein; DNA-binding.
 FT SITE 315 316
 FT FT BREAKPOINT FOR TRANSLOCATION TO FORM THE
 FT FT REP-RET ONCOGENE.
 FT ZN_FING 16 57
 FT ZN_FING 96 127
 FT DOMAIN 368 493
 FT FT B BOX-TYPE.
 FT FT SPRY.
 SQ SEQUENCE 513 AA; 58489 MW; 6F963D9048D8A731 CRC64;

Query Match 29.4%; Score 84; DB 1; Length 513;
 Best Local Similarity 35.6%; Pred. No. 0.0027;
 Matches 16; Conservative 8; Mismatches 17; Indels 4; Gaps 2;

4 CTICSDPFDRVAMDCGHTFHLQCLIOSFETAPSR-TCPCOR 47
 Db 16 CPVLQYF---AEPMMLDGCHNICACIARCGWTAETWVSCPCR 57

RESULT 12
 RAPS_MOUSE
 ID RAPS_MOUSE STANDARD; PRT: 411 AA.
 AC P12672;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 43 kDa receptor-associated protein of the synapse (RAPSYN)
 DE (acetylcholine receptor-associated 43 kDa protein) (43 kDa
 DE postsynaptic protein).
 GN RAPS.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=8928985; PubMed=2737281;
 RA Froehner S.C.;
 RT "Expression of RNA transcripts for the postsynaptic 43 kDa protein in
 RT innervated and denervated rat skeletal muscle.";
 RL FEBS Lett. 249:229-233(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RX MEDLINE=89008468; PubMed=3170600;
 RA Frail D.E., McLaughlin L.L., Mudd J., Merlie J.P.;
 RT "Identification of the mouse muscle 43,000-dalton acetylcholine
 RT receptor-associated protein (RAPSyn) by cDNA cloning.";

RL J. Biol. Chem. 263:15602-15607(1988).
 CC -1- FUNCTION: THOUGHT TO PLAY SOME ROLE IN ANCHORING OR STABILIZING
 CC THE NICOTINIC ACETYLCHOLINE RECEPTOR AT SYNAPTIC SITES. IT MAY
 CC LINK THE RECEPTOR TO THE UNDERLYING POSTSYNAPTIC CYTOSKELETON.
 CC POSSIBLY BY DIRECT ASSOCIATION WITH ACTIN OR SPECTRIN.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF POSTSYNAPTIC
 CC MEMBRANES.
 CC -1- DOMAIN: A CYSTEINE-RICH REGION HOMOLOGOUS TO PART OF THE
 CC REGULATORY DOMAIN OF PROTEIN KINASE C MAY BE IMPORTANT IN
 CC INTERACTIONS OF THIS PROTEIN WITH THE LIPID BILAYER.
 CC -1- SIMILARITY: BELONGS TO THE RAPSYN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL: X15786; CA33789.1; -
 DR EMBL: J03962; AAA40030.1; -
 DR PIR: S04488; S04488.
 DR PIR: A31995; A31995.
 DR MGD: MGI:99422; Rapsn.
 DR InterPro: IPR001237; Postsynaptic.
 DR InterPro: IPR001440; TPR.
 DR InterPro: IPR001841; Znf_fing.
 DR Pfam: PF00515; TPR.6.
 DR PRINTS: PR00217; POSTSYNAPTIC.
 DR PRODOM: PD012428; Postsynaptic.1.
 DR SMART: SM00184; RING.1.
 DR SMART: SM00028; TPR.3.
 DR PROSITE: PS00405; 43_KD_POSTSYNAPTIC.1.
 DR PROSITE: PS00518; ZF_RING.1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KM Synapse; Postsynaptic membrane; Cytoskeleton; Phosphorylation;
 KW Myristate; Zinc-finger.
 FT INT_MET 0 0
 FT ZN_FING 362 402
 FT FT LIPID 1 1
 FT MOD_RES 195 195
 FT MOD_RES 404 404
 FT CONFLICT 343 344
 FT FT DV -> FL (IN REF. 2).
 SQ SEQUENCE 411 AA; 46233 MW; 1085A5C709FDIE56 CRC64;

Query Match 29.2%; Score 83.5; DB 1; Length 411;
 Best Local Similarity 33.3%; Pred. No. 0.0025;
 Matches 15; Conservative 10; Mismatches 15; Indels 5; Gaps 2;

4 CTICSDPF-DHSRDVAMDCGHTFHLQCLIOSFETAPSR-TCPCOR 47
 Db 362 GCLGESIGERNRSLQALPCHIFRLCL-----QNNGRSCPCNR 402

RESULT 13
 Y057_CAEEL
 ID Y057_CAEEL STANDARD; PRT: 235 AA.
 AC Q09463;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 24.9 kDa protein Cl6C10.7 in chromosome III.
 GN Cl6C10.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;


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RA  Lloyd C.;
RL  Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
CC  -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-----
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CC  or send an email to license@isb-sib.ch).
-----
CC  EMBL; 246787; CAAB6745.1; -
CC  Morneprep; C16C10.7; CE01498.
CC  InterPro; IPR000306; Znf_FYVE.
CC  InterPro; IPR001841; Znf_Fing.
CC  Pfam; PF000097; zf-C3HC4; 1.
CC  SMART; SM00064; FYVE; 1.
CC  SMART; SM00184; RING; 1.
CC  PROSITE; PS00518; ZF_RING_1; 1.
CC  PROSITE; PS50089; ZF_RING_2; 1.
CC  Hypothetical protein; Zinc-finger.
CC  ZN_FING 26 67 RING-TYPE.
CC  DOMAIN 121 124 POLY-GLY.
CC  FT 169 172
CC  FT 172 172 POLY-ALA.
CC  SQ SEQUENCE 235 AA; 24915 MW; 21A04AE951F6382A CRC64;

Query Match 29.0%; Score 83; DB 1; Length 235;
Best Local Similarity 37.8%; Pred. NO. 0.0017;
Matches 17; Conservative 6; Mismatches 18; Indels 4; Gaps 2;

OY 4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIOSFEFAP-SRTCPQCR 47
Db 26 CNIC---LDAAKDAVNSLCGHLFCMPCISQMLDTRPNNOVCPCVK 67

RESULT 14
GOLI_DROME STANDARD; PRT; 284 AA.
AC 006003;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Goliah protein (G1 protein).
GN GOL OR G1 OR GL.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE-Embryo;
RX MEDLINE-93216124; Pubmed-8462875;
RA Boucharde M.L., Cote S.;
RT "The Drosophila melanogaster developmental gene g1 encodes a variant
RT zinc-finger-motif protein."
RL Gene 125:205-209(1993).
CC -1- FUNCTION: REGULATION OF GENE EXPRESSION DURING MESODERM FORMATION.
CC -1- PUTATIVE ROLE AS TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: VISCERAL MESODERM AND PRIMORDIA OF SOMATIC
CC MUSCULATURE.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-----
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CC  EMBL; M97204; AAA28582.1; -
CC  PIR; JCI495; JCI495.
CC  FlyBase; FBgn0004919; gol.
CC  InterPro; IPR001841; Znf_Fing.
CC  Pfam; PF00097; zf-C3HC4; 1.
CC  SMART; SM00184; RING; 1.
CC  PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
CC  PROSITE; PS50089; ZF_RING_2; 1.
CC  Developmental protein; zinc-finger; transcription regulation;
CC  DNA-binding; Nuclear protein.
CC  ZN_FING 126 167 RING-TYPE.
CC  DOMAIN 208 259 GLN/PRO/SER-RICH.
CC  SQ SEQUENCE 284 AA; 31973 MW; BCEF2D5EDBA1E2B CRC64;

Query Match 28.7%; Score 82; DB 1; Length 284;
Best Local Similarity 31.4%; Pred. NO. 0.0027;
Matches 16; Conservative 8; Mismatches 17; Indels 10; Gaps 2;

OY 4 CTICSDFFDHSRDVAAMDCGHTFHLQCLIOSFEFAP-SRTCPQCRIOV 50
Db 126 CALCIETAKPYDTIRILPCKEHFHKNCIDPWLE-----HRTCPMKLDV 170

RESULT 15
BML_MOUSE STANDARD; PRT; 324 AA.
AC P25916;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Polycarb complex protein BML-1.
GN BML OR BML-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-91249382; Pubmed-1904009;
RA Haupt Y., Alexander W.S., Barri G., Klincken S.P., Adams J.M.;
RT "Novel zinc finger gene implicated as myc collaborator by
RT retrovirally accelerated lymphomagenesis in E mu-myc transgenic
RT mice."
RL Cell 65:753-761(1991).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE-91249381; Pubmed-1904008;
RA van Lohuizen M., Verbeek S., Scheijen B., Mientjens E.,
RA Gulden H., Berns A.;
RT "Identification of cooperating oncogenes in E mu-myc transgenic mice
RT by provirus tagging."
RL Cell 65:737-752(1991).
CC -1- FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE
CC STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
CC IN ITS EXPRESSIBILITY.
CC -1- SUBUNIT: COMPONENT OF THE CHROMATIN-ASSOCIATED POLYCOMB COMPLEX
CC (PCG).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: DETECTED IN MOST ORGANS WITH HIGH EXPRESSION
CC LEVELS IN THYMUS, HEART, BRAIN AND TESTIS.
CC -1- DISEASE: COOPERATES WITH THE MYC ONCOGENE TO PRODUCE B LYMPHOMAS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-----
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DR EMBL: D90085; BAA1412.1; -
DR EMBL: BC016419; AAH16419.1; -
DR PIR: A37991; A37991.
DR MGI: 99161; Zfp144.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Transcription regulation; Repressor; Zinc-finger; DNA-binding;
KW Nuclear protein; Phosphorylation.
FT ZN_FING 18 57 RING-TYPE.
FT DOMAIN 81 95 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 242 342 PRO/SER-RICH.
FT MOD_RES 237 237 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 334 334 PHOSPHORYLATION (BY CAPK)
FT MOD_RES 334 334 (POTENTIAL).
FT SEQUENCE 342 AA; 37723 MW; C23031B8B9E30108 CRC64;

Query Match 28.7%; Score 82; DB 1; Length 342;
Best Local Similarity 29.2%; Pred. No. 0.0032;
Matches 14; Conservative 14; Mismatches 16; Indels 4; Gaps 2;

OY 3 LCTICSDPFHDSRDVAAMDCGTHFLQCLIOSFETAPSRTPCQRIQV 50
DB 17 MCALCGGFIDATYI--VECHLSFCKTCIVRYLET--NKYCPMCDVOV 60

RESULT 18
ME18_HUMAN
ID ME18_HUMAN STANDARD: PRT: 344 AA.
AC P35227;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-binding protein Mel-18 (zinc finger protein 144).
GN ZNF144 OR ME18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93314969; PubMed-8325509;
RA Ishida A., Asano H., Hasegawa M., Koseki H., Ono T., Yoshida M.C.,
RA Taniguchi M., Kanno M.;
RT "Cloning and chromosome mapping of the human Mel-18 gene which
RT encodes a DNA-binding protein with a new 'RING-finger' motif";
RL Gene 129:249-255(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue-placenta;
RA Strausberg R.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS SPECIFICALLY TO THE
CC DNA SEQUENCE 5'-GACTGAGCT-3'. HAS A TUMOR SUPPRESSOR ACTIVITY.
CC MAY PLAY A ROLE IN CONTROL OF CELL PROLIFERATION AND/OR NEURAL
CC CELL DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: DETECTED IN ALL TISSUE EXAMINED WITH HIGH
CC EXPRESSION FOUND IN PLACENTA LUNG AND KIDNEY AND LOW EXPRESSION,
CC IN LIVER, PANCREAS AND SKELETAL MUSCLE.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL: D13969; BAA03074.1; -
DR EMBL: BC004858; AAH04858.1; -
DR PIR: JN0717; JN0717.
DR MIM: 600346; -
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Transcription regulation; Repressor; Zinc-finger; DNA-binding;
KW Nuclear protein.
FT ZN_FING 18 57 RING-TYPE.
FT DOMAIN 81 95 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 242 344 PRO/SER-RICH.
FT SEQUENCE 344 AA; 37788 MW; A910BCD4C0CE9927 CRC64;

Query Match 28.7%; Score 82; DB 1; Length 344;
Best Local Similarity 29.2%; Pred. No. 0.0032;
Matches 14; Conservative 14; Mismatches 16; Indels 4; Gaps 2;

OY 3 LCTICSDPFHDSRDVAAMDCGTHFLQCLIOSFETAPSRTPCQRIQV 50
DB 17 MCALCGGFIDATYI--VECHLSFCKTCIVRYLET--NKYCPMCDVOV 60

RESULT 19
MKR4_HUMAN
ID MKR4_HUMAN STANDARD: PRT: 485 AA.
AC O13434;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 4 (zinc-finger protein 127-Xp) (ZNF127-Xp).
GN MKR4 OR ZNF127L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hendrich B.D., Longstreet M., Gustashaw K., Nicholls R.D.,
RA Willard H.F.;
RT "An X-linked homologue of the autosomal imprinted gene ZNF127
RT escapes X chromosome inactivation";
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
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DR EMBL: U41315; AAA99070.1; -
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; zf-C3HC4; 1.
DR Pfam: PF00642; zf-C3HC4; 4.
DR SMART: SM00356; ZNF_C3H1; 4.
DR SMART: SM00356; ZNF_C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Zinc-finger; Repeat.
FT ZN_FING 96 114 C3H1-TYPE 1.
FT ZN_FING 125 143 C3H1-TYPE 2.


```

DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 18.8 kDa protein ZK637.14 in chromosome III.
GN ZK637.14
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=92168156; PubMed=1538779;
RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
RA Halloran N., Green P., Thierly-Mieg J., Ou L., Dear S., Coulson A.,
RA Craxton M., Dubin R.K., Berts M., Metzstein M., Hawkins T.,
RA Ainscough R., Waterston R.,
RT "The C. elegans genome sequencing project: a beginning.";
RL Nature 356:37-41(1992).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
CC EMBL: 211115; CAA77447.1; -.
CC PIR: S15788; S15788.
CC WormPep: ZK637.14; CE00432.
CC InterPro: IPR001841; Znf_fing.
CC Pfam: PF00097; zf-C3HC4; 1.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE: PS50089; ZF_RING_2; 1.
CC Hypothetical protein; zinc-finger.
CC ZN_FING 72 134 RING-TYPE.
CC SEQUENCE 161 AA; 18847 MW; F5EP9F3A83A9C027 CRC64;
SQ

```

Query Match 27.8%; Score 79.5; DB 1; Length 161;
 Best Local Similarity 30.0%; Pred. No. 0.0032;
 Matches 21; Conservative 4; Mismatches 22; Indels 23; Gaps 2;

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OY 2 ALCTGSDPFDHSD-----VAAMDCGTFHLOCTIOSFETAPS 40
DB 70 ATCAICDNDNQNVDIPEDHYKEELKIDPTTGTFTVIYMPCKHRHFYCLTLWLEA--Q 127
OY 41 RTCPGCRIOV 50
DB 128 QTCTPTCKOV 137

```

RESULT 25
 ID 2179_HUMAN STANDARD; PRT; 632 AA.
 AC Q9ULX5; O60633;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Zinc finger protein 179 (Brain finger protein).
 GN ZNF179 OR BFP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Seki N., Hattori A., Saito T.;
 RA "Human BFP/ZNF179";
 RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RL

```

RN [2]
RP SEQUENCE OF 33-127 FROM N.A.
RX MEDLINE=96301415; PubMed=8660987;
RA Matsuda Y., Inoue S., Seki N., Hosoi T., Orimo A., Muramatsu M.,
RA Hori T.;
RT "Chromosome mapping of human (ZNF179), mouse, and rat genes for brain
RT finger protein (bfp), a member of the RING finger family.";
RL Genomics 33:325-327(1996).
CC -1- TISSUE SPECIFICITY: Predominantly expressed in brain.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
CC EMBL: AB026054; BAA84698.1; -.
CC EMBL: AF054587; AAC08584.1; -.
CC MIM: 601237; -.
CC InterPro: IPR001841; Znf_fing.
CC Pfam: PF00097; zf-C3HC4; 1.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE: PS50089; ZF_RING_2; 1.
CC Zinc-finger.
CC ZN_FING 57 98 RING-TYPE.
CC SEQUENCE 632 AA; 68354 MW; F8D294815E65ED02 CRC64;
SQ

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Query Match 27.6%; Score 79; DB 1; Length 632;
 Best Local Similarity 34.7%; Pred. No. 0.014;
 Matches 17; Conservative 7; Mismatches 13; Indels 12; Gaps 3;

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OY 4 CTTCSDPFDHSDVAAMDCGTFHLOCTIOSFET----APSRCPGCR 47
DB 57 CSIC---LERRDPIISLDCGHDFCIRC----FSHRRLPGCEPPGCR 98

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RESULT 26
 ID YLBS_CAEEL STANDARD; PRT; 1281 AA.
 AC P46580;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 146.8 kDa protein C34E10.5 in chromosome III.
 GN C34E10.5.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Kirsten J.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- SIMILARITY: TO S.POMBE SKB1 AND YEAST YBR133C.
 CC -----
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 CC -----
 CC EMBL: U10402; AAA19067.1; -.
 CC WormPep: C34E10.5; CE01185.
 DR InterPro: IPR001841; Znf_fing.
 DR

DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein; Transmembrane; Zinc-finger.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 1165 1185 POTENTIAL.
FT ZN_FING 1222 1267 RING-TYPE.
SQ SEQUENCE 1281 AA; 146773 MW; 7027275AB540D04 CRC64;

Query Match 27.3%; Score 78; DB 1; Length 1281;
Best Local Similarity 30.8%; Pred. No. 0.037;
Matches 16; Conservative 12; Mismatches 14; Indels 10; Gaps 2;

OY 4 CTICSDFFHSDRYAAMDCGTHFLQCLIQ-----SFETAPSRRCPCRCRQ 49
Db 1222 CSTCLE---NKNPSALFCGHLFCWTCIQEHAVATSSASTSARCPQCRLE 1269

RESULT 27
REP_MOUSE STANDARD; PRT; 522 AA.
ID REP_MOUSE
AC Q62158;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Zinc-finger protein RFP (Ret finger protein).
GN RFP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=97176437; PubMed=9023983;
RA Cao T., Shannon M., Handel M.A., Etkin L.D.;
RT "Mouse ret finger protein (rfp) proto-oncogene is expressed at
RT specific stages of mouse spermatogenesis.";
RL Dev. Genet. 19:309-320(1996).
CC -1- FUNCTION: MAY FUNCTION IN MALE GERM CELL DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 SPRY DOMAIN.
CC -----
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CC -----
DR EMBL; LA6855; AAA8354.1; -.
DR MGD; MGI:97904; Rfp.
DR InterPro; IPR001870; Gamma_carboxylase.
DR InterPro; IPR003877; SPRY.
DR InterPro; IPR003878; SPRY_domain.
DR InterPro; IPR000315; znf_box.
DR InterPro; IPR001841; znf_fing.
DR Pfam; PF00622; SPRY; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR Pfam; PF00097; zf-C3HC4; 1.
DR PRINTS; PR01406; BBOXZFINGER.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00184; RING; 1.
DR SMART; SM00449; SPRY; 1.
DR PROSITE; PS50119; ZF_BOX; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Zinc-finger; Metal-binding; Nuclear protein; DNA-binding.

FT ZN_FING 25 66 RING-TYPE.
FT ZN_FING 105 136 B_BOX-TYPE.
FT DOMAIN 377 502 SPRY.
SQ SEQUENCE 522 AA; 59550 MW; BFD418DBA13340B7 CRC64;

Query Match 26.9%; Score 77; DB 1; Length 522;
Best Local Similarity 33.3%; Pred. No. 0.021;
Matches 15; Conservative 8; Mismatches 18; Indels 4; Gaps 2;

OY 4 CTICSDFFHSDRYAAMDCGTHFLQCLIQSEFAPSR-TCPQCR 47
Db 25 CPVCLQYF---VEPMMLDCGNICACIARCMGAETNVSCPCR 66

RESULT 28
STES_YEAST STANDARD; PRT; 917 AA.
ID STES_YEAST
AC P32917;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE STES protein.
GN STES OR NUL3 OR YDR103M OR YD8557.12.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93204951; PubMed=8455598;
RA Mukai Y., Harashima S., Oshima Y.;
RT "Function of the ste signal transduction pathway for mating
RT pheromones sustains MAT alpha 1 transcription in Saccharomyces
RT cerevisiae.";
RL Mol. Cell. Biol. 13:2050-2060(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93296161; PubMed=8516289;
RA Perlman R., Yablonski D., Simchen G., Levitzki A.;
RT "Cloning of the STE5 gene of Saccharomyces cerevisiae as a suppressor
RT of the mating defect of cdc25 temperature-sensitive mutants.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5474-5478(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA Mackay V.L., Mathewes S., Bell L., O'Hara P.J.;
RL Submitted (XXX-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=DBG939;
RX MEDLINE=94067004; PubMed=8246877;
RA Iebner E., Dignard D., Hargus D., Horgan L., Whiteaway M.,
RA Thomas D.Y.;
RT "Cloning of Saccharomyces cerevisiae STE5 as a suppressor of a Ste20
RT protein kinase mutant: structural and functional similarity of Ste5
RT to Far1.";
RL Mol. Gen. Genet. 241:241-254(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Murphy L., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE PHEROMONE SIGNAL TRANSDUCTION PATHWAY.
CC IT MEDIATES PHEROMONE SIGNALS ACTING BETWEEN STE20 AND STE11.
CC IT IS ABSOLUTELY REQUIRED FOR PHEROMONE-INDUCED TRANSCRIPTION OF
CC FUS1. MAY PLAY A ROLE IN CELL-CYCLE ARREST IN RESPONSE TO
CC PHEROMONE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: MAY BE REGULATED AT THE PHOSPHORYLATION LEVEL. AND BY THE
CC MATING TYPE OF THE CELL AND DEPENDS ON AN INTACT PHEROMONE-
CC RESPONSE PATHWAY.
CC -1- SIMILARITY: TO YEAST FAR1.
CC -----

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DR EMBL: D12917; BAA02301.1; -
DR EMBL: L01620; AAA35108.1; -
DR EMBL: L23856; AAA35115.1; -
DR EMBL: L07865; AAA16896.1; -
DR EMBL: Z47746; CAA87679.1; -
DR PIR: S30810; S30810.
DR PIR: S39920; S39920.
DR SGD: S0002510; STE5.
DR InterPro: IPR001841; znf_ring.
DR SMART: SM00184; RING; 1.
DR Phosphorylation response.
KW DOMAIN 775 876 ASP/GLU-RICH (ACIDIC).
FT CONFLICT 331 332 LG -> W (IN REF. 2).
FT CONFLICT 341 343 NSI -> TLS (IN REF. 2).
FT CONFLICT 821 821 A -> R (IN REF. 1).
SQ SEQUENCE 917 AA; 102726 MW; 0435BDA0196BD26F CRC64;

Query Match 26.9%; Score 77; DB 1; Length 917;
Best Local Similarity 30.4%; Pred. No. 0.036;
Matches 17; Conservative 8; Mismatches 21; Indels 10; Gaps 2;

OY 2 ALCTICSDFFDHSR--DVAAMDGHFTHLOCLIOSEFTAPSRT-----CPQCR 47
DB 175 ASCTLCDEPIENRRKKEIIEIACGHLSHQECILISFETSKADYRAFPCTCK 230

RESULT 29
CBLB_HUMAN STANDARD; PRT; 982 AA.
AC 013191; Q13192; Q13193;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Signal transduction protein CBL-B (SH3-binding protein CBL-B).
GN CBLB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=95303504; PubMed=7784085;
RA Keane M.M., Rivero-Lezcano O.M., Mitchell J.A., Robbins K.C.,
RA Lipkowitz S.,
RT Cloning and characterization of cbl-b: a SH3 binding protein with
RT homology to the c-cbl proto-oncogene.";
RL Oncogene 10:2367-2377(1995).
CC -1- SUBUNIT: INTERACTS WITH SH3 DOMAIN PROTEINS FYN, FGR AND PLCG1.
CC -1- SUBCELLULAR LOCATION: Nucleus (Potential).
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A LONG FORM (SHOWN HERE),
CC TRUNCATED ISOFORM 1 AND TRUNCATED ISOFORM 2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, KIDNEY, SPLEEN, AND TESTIS,
CC AS WELL AS FETAL BRAIN AND LIVER AND HEMATOPOIETIC CELL LINES, BUT
CC NOT IN ADULT BRAIN, LIVER, PANCREAS, SALIVARY GLAND, OR SKELETAL
CC MUSCLE.
CC -1- PTM: PHOSPHORYLATED ON TYROSINES.
CC -1- SIMILARITY: CONTAINS 1 UBA-DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RING-DOMAIN.
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DR EMBL: U26710; AAB09291.1; -
DR EMBL: U26711; AAB09292.1; -
DR EMBL: U26712; AAB09293.1; -
DR HSSP: P22681; IBA7.
DR MIM: 604491; -
DR InterPro: IPR003153; CBL_N.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR000449; UBA.
DR InterPro: IPR001841; znf_ring.
DR Pfam: PF02262; CBL_N; 1.
DR Pfam: PF02761; CBL_N2; 1.
DR Pfam: PF02762; CBL_N3; 1.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00252; SH2; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS00089; ZF_RING_2; 1.
DR KW Nuclear protein; zinc-finger; NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 116 119
FT ZN_FING 373 412
FT ZN_FING 477 701
FT DOMAIN 931 970
FT DOMAIN 812 982 UBA.
FT VARSPPLIC 767 770 MISSING (IN TRUNCATED ISOFORM 1).
FT VARSPPLIC 771 982 DVED -> YTRI (IN TRUNCATED ISOFORM 2).
SQ SEQUENCE 982 AA; 109479 MW; 038D4965DAFB98CB CRC64;

Query Match 26.9%; Score 77; DB 1; Length 982;
Best Local Similarity 31.2%; Pred. No. 0.038;
Matches 15; Conservative 11; Mismatches 18; Indels 4; Gaps 2;

OY 3 ICTICSDFFDHSRDVAAMDGHFTHLOCLIOSEFTAPSRTCPQCRIOY 50
DB 372 LCKTCA--ENDKDVKTEPCGHLMTCTSL-TAWQESDGGCPFCRET 415

RESULT 30
MKR2_HUMAN STANDARD; PRT; 416 AA.
AC Q9H000; Q9HRY1; Q9BUY2;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 2 (HSPC070).
GN MKR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=21481893; PubMed=11597136;
RA Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls R.D.,
RA "Phylogenetic conservation of the makorin-2 gene, encoding a multiple
RT zinc-finger protein, antisense to the raf1 proto-oncogene.";
RL Genomics 77:119-126(2001).
CC [2]
CC SEQUENCE FROM N.A.
CC MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-D., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.,
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";


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RL Genome Res. 10:1546-1560(2000).
RN [3]
RP SEQUENCE OF 44-416 FROM N.A.
RC TISSUE-Eye;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- TISSUE SPECIFICITY: Widely expressed.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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CC -----
DR EMBL: AF302084; AAC30426.1; -
DR EMBL: AF277170; AAC27595.1; -
DR EMBL: AF277164; AAC27595.1; JOINED.
DR EMBL: AF277165; AAC27595.1; JOINED.
DR EMBL: AF277166; AAC27595.1; JOINED.
DR EMBL: AF277167; AAC27595.1; JOINED.
DR EMBL: AF277168; AAC27595.1; JOINED.
DR EMBL: AF277169; AAC27595.1; JOINED.
DR EMBL: AF161555; AAF29042.2; -
DR EMBL: BC001799; AAH01799.1; -
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf-CTH.
DR Pfam: PF00097; Zf-C3HC4; 4.
DR Pfam: PF00642; Zf-CCCH; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf-C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Zinc-finger; Repeat.
FT ZN_FING 8 C3H1-TYPE 1.
FT ZN_FING 37 C3H1-TYPE 2.
FT ZN_FING 171 C3H1-TYPE 3.
FT DOMAIN 193 222 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 238 292 RING-TYPE.
FT ZN_FING 327 347 C3H1-TYPE 4.
FT CONFLICT 186 186 F -> V (IN REF. 2 AND 3).
FT CONFLICT 278 278 K -> E (IN REF. 2).
SQ SEQUENCE 416 AA; 46988 MW; 02B6B7ABBD382DDC CRC64;

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RA Gray T.A., Azama K., Whitmore K., Min A., Abe S., Nicholls R.D.;
RT "Phylogenetic conservation of the makorin-2 gene, encoding a multiple
RT zinc-finger protein, antisense to the raf1 proto-oncogene.";
RL Genomics 77:119-126(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischman W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC -----
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CC -----
DR EMBL: AF277171; AAC27596.1; -
DR EMBL: AK011295; BAB27523.1; -
DR MGD: MGI:1914277; Mkrn2.
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; Znf-CTH.
DR Pfam: PF00097; Zf-C3HC4; 4.
DR Pfam: PF00642; Zf-CCCH; 1.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; Znf-C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Zinc-finger; Repeat.
FT ZN_FING 8 C3H1-TYPE 1.
FT ZN_FING 37 C3H1-TYPE 2.
FT ZN_FING 171 C3H1-TYPE 3.
FT DOMAIN 193 222 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 238 292 RING-TYPE.
FT ZN_FING 327 347 C3H1-TYPE 4.
FT CONFLICT 181 181 L -> F (IN REF. 2).
SQ SEQUENCE 416 AA; 46562 MW; 5F268EB9D9A6C9F CRC64;

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Query Match 26.7%; Score 76.5; DB 1; Length 416;
Best Local Similarity 28.1%; Pred. No. 0.019;
Matches 16; Conservative 10; Mismatches 20; Indels 11; Gaps 2;
QY 3 LCTICSDFF-----DHSRDVAAMDCGTFHLOCLIQ-----SETPASRTPCPCRI 48
Db 237 VCSICMEVILEKASASRRRFGILSNCHTYCLSCIRQWCAKQEPENPIKSCPECRV 293

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Query Match 26.7%; Score 76.5; DB 1; Length 416;
Best Local Similarity 28.1%; Pred. No. 0.019;
Matches 16; Conservative 10; Mismatches 20; Indels 11; Gaps 2;
QY 3 LCTICSDFF-----DHSRDVAAMDCGTFHLOCLIQ-----SETPASRTPCPCRI 48
Db 237 VCSICMEVILEKASASRRRFGILSNCHTYCLSCIRQWCAKQEPENPIKSCPECRV 293

```

```

RESULT 31
MKR2_MOUSE STANDARD; PRT; 416 AA.
ID MKR2_MOUSE
AC QSERV1; Q9D0L9;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 2.
GN MKRn2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21481893; PubMed=11597136;

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RESULT 32
TTTC3_HUMAN STANDARD; PRT; 2025 AA.
ID TTTC3_HUMAN

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DR EMBL: AF192786; AAF17489.1; -
DR InterPro: IPR001395; AldoKetRed.
DR InterPro: IPR000571; Zf-CCCH.
DR InterPro: IPR001841; ZnF_RING.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR Pfam: PF00642; Zf-CCCH; 4.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; ZnF_C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Zinc-finger; Repeat.
FT ZN_FING 57 75 C3H1-TYPE 1.
FT ZN_FING 86 104 C3H1-TYPE 2.
FT ZN_FING 210 228 C3H1-TYPE 3.
FT DOMAIN 232 259 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 277 331 RING-TYPE.
FT ZN_FING 366 386 C3H1-TYPE 4.
SQ SEQUENCE 478 AA; 52905 MW; CB2D9B147433853E CRC64;

Query Match 25.7%; Score 73.5; DB 1; Length 478;
Best Local Similarity 28.1%; Pred. No. 0.052;
Matches 16; Conservative 11; Mismatches 19; Indels 11; Gaps 2;

Y 3 LCTICSDFF-----DHSRDVAMDCGTHFLQCL-----IQSFETAPSRFCPCRI 48
Db 276 VCGICMEVVEKAMPSERRFGILSNCHTYCLCKIRKWSAKOFESKTIKSCPECRI 332

RESULT 37
MKRL_MOUSE
ID MKRL_MOUSE STANDARD; PRT; 481 AA.
AC O90X6;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 1.
GN MKRN1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_Taxid=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20304755; PubMed=10843807;
RA Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Smithwick M.J.,
RA Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;
RA "The ancient source of a distinct gene family encoding proteins
RT featuring RING and C(3)H zinc-finger motifs with abundant expression
RT in developing brain and nervous system.";
RL Genomics 66:76-86(2000).
RL
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGERS.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC
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DR EMBL: AF192785; AAF17488.1; -
DR MGD; MGI:1859353; Mkrnl.
DR InterPro: IPR000571; Zf-CCCH.

DR InterPro: IPR001841; ZnF_RING.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR Pfam: PF00642; Zf-CCCH; 4.
DR SMART: SM00184; RING; 1.
DR SMART: SM00356; ZnF_C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Zinc-finger; Repeat.
FT ZN_FING 61 79 C3H1-TYPE 1.
FT ZN_FING 90 108 C3H1-TYPE 2.
FT ZN_FING 214 232 C3H1-TYPE 3.
FT DOMAIN 236 263 MAKORIN-TYPE CYS-HIS.
FT ZN_FING 281 335 RING-TYPE.
FT ZN_FING 370 390 C3H1-TYPE 4.
SQ SEQUENCE 481 AA; 53008 MW; B6BDBE5E765CEAE CRC64;

Query Match 25.7%; Score 73.5; DB 1; Length 481;
Best Local Similarity 28.1%; Pred. No. 0.052;
Matches 16; Conservative 11; Mismatches 19; Indels 11; Gaps 2;

Y 3 LCTICSDFF-----DHSRDVAMDCGTHFLQCL-----IQSFETAPSRFCPCRI 48
Db 280 VCGICMEVVEKAMPSERRFGILSNCHTYCLCKIRKWSAKOFESKTIKSCPECRI 336

RESULT 38
MKRL_HUMAN
ID MKRL_HUMAN STANDARD; PRT; 482 AA.
AC O90HC7; O90EZ7; O90HGO;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Makorin 1.
GN MKRN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN NCBI_Taxid=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20304755; PubMed=10843807;
RA Gray T.A., Hernandez L., Carey A.H., Schaldach M.A., Smithwick M.J.,
RA Rus K., Marshall Graves J.A., Stewart C.L., Nicholls R.D.;
RA "The ancient source of a distinct gene family encoding proteins
RT featuring RING and C(3)H zinc-finger motifs with abundant expression
RT in developing brain and nervous system.";
RL Genomics 66:76-86(2000).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis.
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Well B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Amorge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
RA Lauber J., Duestenhoef A., Beyer A., Koehler K., Strack N.,
RA Meyers H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wandt R., Korn B., Klein M., Poustka A.;
RA "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs.";
RL Genome Res. 11:422-435(2001).
RL
CC -1- TISSUE SPECIFICITY: Ubiqutious.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGERS.
CC -1- SIMILARITY: CONTAINS 4 C3H1-TYPE ZINC FINGERS.
CC
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DR EMBL: AF192784; AAF17487.1; -

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DR EMBL: AF192793; AAF18979.1; -.
DR EMBL: AF192789; AAF18979.1; JOINED.
DR EMBL: AF192790; AAF18979.1; JOINED.
DR EMBL: AF192791; AAF18979.1; JOINED.
DR EMBL: AF192792; AAF18979.1; JOINED.
DR EMBL: AL136812; CAB6746.1; -.
DR InterPro: IPR000571; Znf-CCCH.
DR InterPro: IPR001841; Znf-CCCH.
DR Pfam: PF00097; Zf-CCCH; 1.
DR Pfam: PF00642; Zf-CCCH; 1.
DR SMART: SM00184; RING_1.
DR SMART: SM00356; Znf_C3H1; 4.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR ZINC-finger Repeat; Polymorphism.
KW ZN-FING 61 79 C3H1-TYPE 1.
FT ZN-FING 90 108 C3H1-TYPE 2.
FT ZN-FING 214 232 C3H1-TYPE 3.
FT DOMAIN 236 263 MAKORIN-TYPE CYS-HIS.
FT ZN-FING 281 335 RING-TYPE.
FT ZN-FING 370 390 C3H1-TYPE 4.
FT VARIANT 243 243 L->V.
FT CONFLICT 395 396 /FTID-VAR_012161.
SQ SEQUENCE 482 AA; 53363 MW; C993DECDD131691C CRC64;

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Query Match 25.7%; Score 73.5; DB 1; Length 482;
Best Local Similarity 28.1%; Pred. No. 0.052;
Matches 16; Conservative 11; Mismatches 19; Indels 11; Gaps 2;

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QY 3 LCTICSDFF-----DHSRDVAAADCGHTFHLOCL-----IQSEFTAPSRCTPOCR 48
Db 280 VCGICMEVVEKANKNSERRFCILSCNHTYCLCKIRKRSKQKFSKIKSCPECR 336

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RESULT 39
YHBO_YEAST STANDARD; PRT; 585 AA.
AC P38748;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 67.5 kDa protein in PRPS4-STE20 intergenic region.
GN YH1010C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RX MEDLINE=94378003; Pubmed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favell A., Fulton L., Galtung S., Gelsel C., Kirsten J.,
RA Kicaba T., Hillier L., Jiler M., Johnston L., Langston Y.,
RA Lettrelle P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Travaskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaadin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).
CC -1- SIMILARITY: TO C.ELEGANS EED8.9 AND S.POMBE SPAC1658.13.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: U11582; CAB34905.1; -.
DR PIR: S46825; S46825.
DR SGD: S0001002; YH1010C.
DR InterPro: IPR001841; Znf_fing.
DR InterPro: IPR001607; Zf-UBP.
DR Pfam: PF00097; Zf-CCCH; 1.
DR Pfam: PF02148; Zf-UBP; 1.
DR SMART: SM00280; RING_1.
DR SMART: SM00184; Znf-UBP; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE-NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Hypothetical protein; zinc-finger.
FT ZN-FING 240 280 RING-TYPE.
SQ SEQUENCE 585 AA; 67503 MW; 88F670CC73A1263 CRC64;

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Query Match 25.7%; Score 73.5; DB 1; Length 585;
Best Local Similarity 33.3%; Pred. No. 0.063;
Matches 15; Conservative 6; Mismatches 19; Indels 5; Gaps 2;

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QY 4 CTICSDFFD-HSRDVAADCGHTFHLOCLIOSFETAPSRCTPOCR 47
Db 240 CPVCLERMDSFTGLVTPCQHTFHCOCL---NKKMSRCPVCR 280

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RESULT 40
RN12_MOUSE STANDARD; PRT; 600 AA.
AC Q9WTV7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RING finger protein 12 (LIM domain interacting RING finger protein)
DE (RING finger LIM domain-binding protein) (R-LIM).
GN RNF12 OR LIM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Bach I.;
RT "Opposing developmental functions of positive and negative
RT coregulators of LIM homeodomain factors."
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP FUNCTION.
RX MEDLINE=9364422; Pubmed=10431247;
RA Bach I., Rodriguez-Esteban C., Carriere C., Bhushan A., Krones A.,
RA Rose D.W., Glass C.K., Andersen B., Izpisua Belmonte J.C.,
RA Rosenfeld M.G.;
RT "RIM inhibits functional activity of LIM homeodomain transcription
RT factors via recruitment of the histone deacetylase complex."
RL Nat. Genet. 22:394-399(1999).
CC -1- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN
CC TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE
CC DEACETYLASE COREPRESSOR COMPLEX.
CC -1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
DR EMBL: AF069992; MAD34209.1; -.
DR MGD: MG1:1342291; Rnf12.
DR InterPro: IPR001841; Znf_fing.
DR Pfam: PF00097; Zf-CCCH; 1.

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DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Transcription regulation; zinc-finger.
 FT DOMAIN 415 484 SER-RICH.
 FT ZN_FING 546 587 RING-TYPE.
 FT DOMAIN 447 461 POLY-SER.
 SO SEQUENCE 600 AA; 66470 MW; E68299530126E41D CRC64;

Query Match 25.5%; Score 73; DB 1; Length 600;
 Best Local Similarity 27.3%; Pred. No. 0.075;
 Matches 12; Conservative 10; Mismatches 20; Indels 2; Gaps 1;

Oy 4 CTICSDFFDHSRDVAMDCGHTFHQCLIOSFETAPSRTPQCR 47
 |::| : : | | | : : : | | | |
 Db 546 CSVCTEYEGDKLRKLPCHSHFVHCIDRWL--SENSTCPICR 587

Search completed: September 4, 2002, 16:17:41
 Job time: 500 sec

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